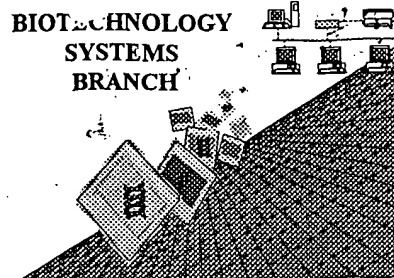


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/887,272
Source: OIP
Date Processed by STIC: 7/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/887,272

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☒ Skipped Sequences
 (NEW RULES) Sequence(s) 69 and many more missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/887,272

DATE: 07/30/2001

TIME: 11:31:15

Input Set : D:\382636.txt

Output Set: N:\CRF3\07302001\I887272.raw

Does Not Comply
Corrected Diskette Needed*error*
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E-->

4 <110> APPLICANT: Hou, Yu-Ming
 5 Quan, Sheng
 6 Chang, Hur-Song
 7 Zhu, Tong
 8 Whitham, Steve
 9 Goff, Steve
 10 Glazebrook, Jane
 11 Chen, Wenquiong
 12 Katagiri, Fumiaki
 13 Xie, Zhiyi
 14 Tao, Yi
 15 Zou, Guangzhou
 16 Cooper, Bret
 18 <120> TITLE OF INVENTION: PLANT GENES INVOLVED IN DEFENSE AGAINST PATHOGENS
 21 <130> FILE REFERENCE: 1360.003US2
 23 <140> CURRENT APPLICATION NUMBER: US/09/887,272
 23 <141> CURRENT FILING DATE: 2001-06-22
 23 <150> PRIOR APPLICATION NUMBER: 60/213,634
 24 <151> PRIOR FILING DATE: 2000-06-23
 26 <150> PRIOR APPLICATION NUMBER: 60/214,926
 27 <151> PRIOR FILING DATE: 2000-06-23
 29 <150> PRIOR APPLICATION NUMBER: 60/261,320
 30 <151> PRIOR FILING DATE: 2001-01-12
 32 <150> PRIOR APPLICATION NUMBER: 60/264,353
 33 <151> PRIOR FILING DATE: 2001-01-26
 35 <150> PRIOR APPLICATION NUMBER: 60/273,879
 36 <151> PRIOR FILING DATE: 2001-03-07
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 40 <170> SOFTWARE: FastSEQ for Windows Version 4.0

5727 shown (px 28-30)

ERRORED SEQUENCES

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 74 <212> TYPE: DNA
 75 <213> ORGANISM: Arabidopsis thaliana
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RAW SEQUENCE LISTING

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DATE: 07/30/2001

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RAW SEQUENCE LISTING

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DATE: 07/30/2001

TIME: 11:31:15

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RAW SEQUENCE LISTING

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DATE: 07/30/2001

TIME: 11:31:15

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RAW SEQUENCE LISTING

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DATE: 07/30/2001

TIME: 11:31:15

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1440/1434

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1711 tcaggaacaa caagagaat tgcagctcag tttcaatcaa gtggttttga tagacacttg 240
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(1881)/880

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2868 ggagagaaac aagcgataag caattacaat aaacatcttg tcaactgctta taaagcagga 840
2870 gtcattgaag gtggttcaac tggattgggt cttggaacgc tctttcttgt agtcttttgt 900

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RAW SEQUENCE LISTING

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Output Set: M:\CRF3\07302001\I887272.raw

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2876	tcgccttgct	taagcgcatt	tgcagctgga	caagccgcgg	cttacaagat	gtttgagaca	1080
2878	attgagagaa	gacctaacat	agattcttat	agtacaaatg	gtaaagtttt	ggatgacatt	1140
2880	aaggagata	ttgagctcaa	agatgtttac	tttacttacc	cagcgagacc	cgatgagcaa	1200
2882	atatttcgcg	gattctctct	gtttatctcg	agtggatcaa	cggtggcttt	agttggacaa	1260
2884	agtgggagcg	ggaaatctac	tgttgtgagt	ctgattgaga	ggttttacga	tccacaagct	1320
2886	ggtgacgttc	tcatagatgg	tattaactta	aaagagtttc	agctaaaatg	gattagaagc	1380
2888	aagattggac	ttgtgagtca	agaaccagtt	ttgttctactg	caagcatcaa	ggataacatt	1440
2890	gcgtacggca	aagaagacgc	aacaaccgaa	gagattaaag	cagctgcaga	gctagcaaac	1500
2892	gcatctaaat	ttgtggataa	gctaccacag	ggtttgata	caatggttgg	agaacatggt	1560
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2896	ccaagaatct	tacttttaga	tgaagtctaca	agcgcgcttg	atgcagaatc	tgagagagtg	1680
2898	gttcaagaag	gccttgatag	aattatggtt	aaccggacta	ctggtgtggt	cgctcatcgg	1740
2900	ttaagcactg	tgcgaatgc	ggatatgata	gctgtgatcc	accaaggcaa	gatcgctcag	1800
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2964	caggacgcgc	tagaccgtgt	tatggtaaac	cggactacga	ttgtggtagc	tcaccgggta	3720
2966	tcgacgatta	agaatgctga	cgtaattgcc	gtcgtaaga	acggcgatc	cgttgagaaa	3780
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RAW SEQUENCE LISTING

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3861 3860

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3272 <212> TYPE: DNA

3273 <213> ORGANISM: Arabidopsis thaliana

3275 <400> SEQUENCE: 64

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3280	gtgaacatga	gcagagtaga	agatattcag	acttttgagg	atttcgcata	gccgttgctt	180
3282	gaggttcttg	agtcttttgg	ctcggatgat	aaagtagtcc	tcgtcgcgca	tagcctcggt	240
3284	ggaataccgg	ctgctcttgc	agccgacatg	tttcctagta	aaatctctgt	tgctgtcttc	300
3286	gttacttctt	ttatgcccg	cacaacgaat	ccaccttctt	acgtgttcga	aaagtttctc	360
3288	ggaagcatta	cagaagaaga	acgtatggac	ttcgagttag	ggagctatgg	aacagatgac	420
3290	catccactaa	agactgcttt	tcttggaact	aactacttga	agaatatgta	tctactttct	480
3292	cctatcgaag	attatgaatt	ggccaaaatg	ttgatgagag	tcacaccggc	tattactagt	540
3294	aatctgacgg	ggactaaaag	cttaacggca	caaggatatg	gatcgattag	tcgtgtgtat	600
3296	atcgtatcgc	gagaagataa	gggtatacgt	gtagatttcc	aacgatggat	gattgagaac	660
3298	tctccggtta	aagaagtgat	ggagatcaaa	gatgcagatc	atatgcctat	gttttccaag	720

E--> 3300 cctcatgaac tctgtgacg tcttctaaag attgctgata aatatcccta

771 770

3336 <210> SEQ ID NO: 66

3337 <211> LENGTH: 1674

3338 <212> TYPE: DNA

3339 <213> ORGANISM: Arabidopsis thaliana

3341 <400> SEQUENCE: 66

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3346	atctccgtta	acaccaacaa	taatgatgat	tccttattaa	ctacgagcca	gatttgccat	180
3348	ggagctcacg	accaagactc	atgccaaagt	ctcttctcgc	aattcacgac	gttgctcgtc	240
3350	tcaaagctca	accgccttga	cctattgcac	gtgtttttga	agaactcggg	gtggcggtt	300
3352	gagagcacga	tgaccatggt	gagcgaggct	aggatccgct	cgaacgggtg	tagagacaag	360
3354	gcaggttttg	ctgactgcga	ggagatgatg	gacgtatcaa	aggatcggat	gatgagttcg	420
3356	atggaggaac	ttcgcggagg	aaactataat	cttgagtcac	actcaaacgt	tcatacttgg	480
3358	ctgagcagtg	tgcttacaaa	ctacatgaca	tgtttagaaa	gtattagtga	tgctccgctc	540
3360	aactctaagc	aaatagtcaa	gccacaactc	gaggacttgg	tttctagggc	aagagtggct	600
3362	ctagccatct	ttgtctccgt	cttgccctgcc	agagacgac	tcaaaatgat	catttccaat	660
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3370	aaaggggttt	acaaagaaac	tattgacata	ggaaagaaaa	agaagaactt	aatgcttgtt	900
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3374	accttcagat	cagccactgt	tgctgccaat	ggagacgggt	ttatggcaca	agacatatgg	1020
3376	ttccaaaaca	ctgcagggcc	ggcaaagcac	caggctgtgg	ctctacgagt	gagtgtgat	1080
3378	caaactgtta	taaatcggtg	tcgcatagat	gcgtatcaag	acacgctcta	cactcacacg	1140
3380	ttgagacaat	tctaccgcga	cagctacatc	accggtaccg	tagatttcat	cttcggaaac	1200
3382	tctgctgtgg	tattccagaa	ctgcgacatc	gtggcacgaa	atcctggagc	tgggcaaaag	1260
3384	aacatgttaa	cggctcaagg	acgggaggat	cagaaccaga	acaccgccat	ttcgatccaa	1320
3386	aaatgtaaga	taacggctag	ttcggatctt	gtcctgttaa	aaggatctgt	gaaaacgttc	1380
3388	cttggtcgac	cgtggaagtt	gtactcaaga	acagtgatca	tgcagtcttt	cattgacaac	1440
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 E--> 3396 caaggaggat tatggttgaa acccaactgga gttactttcc aagagtggct ttga 1680/674
 3440 <210> SEQ ID NO: 68
 3441 <211> LENGTH: 3621 3620
 3442 <212> TYPE: DNA
 3443 <213> ORGANISM: Arabidopsis thaliana
 3445 <400> SEQUENCE: 68
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 3448 gatagaatta gtgatgagca agtagtgaag aatgagttgg tgagatctga tgaagtaagg 120
 3450 gatgataacg aggacgaggt ttttgaggaa gcgattggtt cagagaatga tgagcaggag 180
 3452 gaggaggagg atccaaaacg tgaattgttt gaatctgatg atttgccttt agtggaact 240
 3454 cttaaaagtt ctatggttga gcatgaagtg gaggattttg aagaggcagt gggtgatttg 300
 3456 gatgaaacga gtagcaatga agggggtggt aaagatttta cggctgttgg agagagccat 360
 3458 ggtgcgggag aggctgaatt tgatgttttg gctactaaaa tgaatgggtg taagggggaa 420
 3460 ggaggtggag gtggttctta tgataaagtt gaatcgagct tggatgttgt tgataccact 480
 3462 gagaatgcta catcaactaa tactaatggt tccaatttag cagctgagca tgtgggtatt 540
 3464 gaaaacggaa agactcattc ttttttggga aatggaatcg cctctcctaa aaataaagaa 600
 3466 gtggtggctg aagttatccc taaagatgat gggattgagg aaccatggaa tgatggcatt 660
 3468 gaagtcgata attgggagga aagagttgat ggcatacaga cagaacaaga ggttgaggaa 720
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3536 cgtaagatgt ttaagaaatt tgctgcagag attaaagatt tgcctgatgg gtatagttaa 2760
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3564 caacttgcta tggttgcgat tgttctcttc ttcaagaagc tacttagtta ttattaccgc 3600
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3572 <213> ORGANISM: Arabidopsis thaliana
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3577 tttcccaggt catgctctca gagaaattct ctgtctttga ttcaatgcga tataaaagag 120
3579 agatctttcg gagagtctat gacgatcacg aatcgtggat tgagttttaa gacgaatgtg 180
3581 tttgagcaag ctgcttctgt gactggagac tgttcttatg atgaaacttc agctaaagca 240
3583 cgttctcatg ttgttcgaga agataagatt ggtgtcttgc ttttgaattt aggtggctcc 300
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3591 ataactgatg agcaagcgga tgctattaag atgtctttgc aagcgaagaa cattgctgct 540
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3597 acaacgggtt caagcatacg cgttctccaa gatttattca ggaaagatcc gtacctagct 720
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3605 cagatggaag agtgattga cttgataatg gaagagctaa aagccagagg ggttcttaac 960
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3609 gatgaggttc ttgtcgacct tggtaagagt ggtgttaaga gtctactagc cgttccagtc 1080
3611 agtttcgtga gtgagcacat tgagacactt gaggagatag acatggagta tagggaatta 1140
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3615 ttcatacccg acttagctga tgcagtgata gaatacttc cttcagcaga agcaatgtca 1260
3617 aacccaaatg cagtggttga ctcagaagat agcgagtcgt cagatgcttt cagttacatt 1320
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3624 <210> SEQ ID NO: 71

3625 <211> LENGTH: 1734

3626 <212> TYPE: DNA

3627 <213> ORGANISM: Arabidopsis thaliana

3629 <400> SEQUENCE: 71

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3634 gcctcggcgt ttcagtagca aggtgcaaca agtgaagggt gcaagtctcc aactatatgg      180
3636 gatcacttca gcctcacgta tccagaaaagg accaaaatgc ataatgcaga tgtagcaatt      240
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3674 gaagaacttc acaaagctat agtggaagat ggggtgtgac taagaggata ttacgcattg      1380
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3684 atggcaatga accaatcgag gagagatgag gagaataatc gttgctcctt tgattttcct      1680
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1734

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RAW SEQUENCE LISTING

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4294 gatcaaaaaca acaaggaaga tttcgtctct actacagctg cggagatgcc aacctctccg 420
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4298 gacatctcca atagcaacaa agactccgcg acgtcatccg aagatgttct tgcaattata 540
4300 gatgagagct tttggtcaga agtggatttg atggactgtg acatttcagg aaatgagaag 600
4302 aatgagaaaa agatagagaa ttgggagggc tcactagata gaaacgataa gggatataac 660
4304 catgacatgg agttttggtt tgaccatctc actagtagta gttgtataat tggagaaatg 720
E--> 4306 tccgacattt ctgagttttg 741 740
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4533 <213> ORGANISM: Arabidopsis thaliana
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(3261) 326.0

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RAW SEQUENCE LISTING

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DATE: 07/30/2001

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RAW SEQUENCE LISTING

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 8704 aggctcgaaa gcgtgaagtt tcaaagtatc aggagtgcg ctaagggtgg tggaaacagta 420
 8706 actacagttg gaggaatcat ggtcatgaca cttgtaaaag gtccagctct tgacctcttc 480
 8708 tggactaaag gaccctctgc acagaacaca gttgggaccg atattcatag ctccatcaaa 540
 8710 ggtgcagttt tagtcacaat tgggtgcttc agctatgcat gtttcatgat actacaagca 600
 8712 atcacattga agacttacct tgcagagctc tctctcgcaa catggatatg cctaataagg 660
 8714 acaatagagg gagtagttgt agcattagtg atggagaaa gaaatcctag cgtgtgggcc 720
 8716 attggttggg aactaaact tcttacaatc acctatagtg ggatagtgtg ctcagcgctt 780

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/887,272

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Input Set : D:\382636.txt

Output Set: N:\CRF3\07302001\I887272.raw

8718 gggtactaca ttggaggagt ggtgatgaaa accagaggtc ctgtgtttgt aacagctttc 840
 8720 aaacctcttt gtatgatcgt tgtggcgatt atgtcgagca tcatctttga tgagcagatg 900
 8722 tacctcgga gggctcttgg tgctacggtc atatgtgtag gtctatacct tgtgatatgg 960
 8724 ggcaaagcca aagattatga atatcctagc acgccgcaaa tagatgatga cttagcacia 1020
 E--> 8726 gcaaccacaa gcaagcaaaa agaacaaaga agaacagtga tagaatcagt ctaa (1080)/094

9643 <210> SEQ ID NO: 204

9644 <211> LENGTH: 2037

9645 <212> TYPE: DNA

9646 <213> ORGANISM: Arabidopsis thaliana

9648 <400> SEQUENCE: 204

9649 atgtcttctc tcttcccttt catattcctt tctcttttct cattcctcac tagcttcaga 60
 9651 gcttctgctc aagatcctcg tttcctagcc tattattgtc caaatgcaac aacttactca 120
 9653 agtaacagca cttacttgac caatcttaaa acccttttgt cctctctctc ttcccgcaac 180
 9655 gcctcttact ccaccggatt ccaaaacgcc acggtgggac aagcccttga cagggtcacc 240
 9657 ggacttttcc tttgccgggg agacgtctcg ccggaaaagag aagctgtgtt ctattacgag 300
 9659 gagtgcatac tcagatactc tcacaagaat attctatcga cggccattac aaacgaagga 360
 9661 gaatttatct tgaggaaccc caatcatatt tctcctattc aaaatcaa ataccagttt 420
 9663 actaatttgg tgttatctaa tatgaaccaa attgccatcg aagcagccga caatcctaga 480
 9665 aaattctcta cgataaagac cgaattgacc gcactccaga ctttctacgg gcttgttcaa 540
 9667 tgcactcctg atctttcaag acaaaactgc atgaactgtc tgacaagttc catcaataga 600
 9669 atgccatttt ctagaattgg agcaagacag ttttggccaa gttgtaattc aaggtagcag 660
 9671 ctttacgatt tctacaacga aaccgccatt ggtacaccac caccgccgct gcctccgttg 720
 9673 gcactctcct cactatctgg tgaacagttt cttctacctt tgccctgtt acttgatctt 780
 9675 tgcagtatta ccaatatgga acgcagaatg atctgtttaa acgcagataa aagtgggaat 840
 9677 tcaaatgtgg tcgtggtagc cgttgtttgt cctatcatag tcgtgttct gattttcata 900
 9679 gctggttatt gtttctttgc aaagagggca aagaagactt atggcacaac acctgcttta 960
 9681 gatgaagatg ataaaaaac catagagtcg ctgcaacttg attatagagc aattcaagct 1020
 9683 gcaacaaatg atttttcaga gaataataaa attggtcgag gaggttttgg tgacgtttac 1080
 9685 aagggtacat tttcaaattg aaccgaagtt gcagtgaaga gactgtcgaa aacatcagaa 1140
 9687 caaggtgaca cagaattcaa gaacgaggtt gtagttgttg caaatcttcg gcacaaaaat 1200
 9689 cttgttagga ttctcggaat ttctatgaaa cgagaagaaa ggatatttgt ctacgagtat 1260
 9691 gtagaaaata aaagccttga taacttccta tttgatcctg caaagaaaagg tcagttgtac 1320
 9693 tggacacagc gataccatat cattggtggg attgctagag ggatcctata tcttcatcaa 1380
 9695 gattcacgac tcacaatcat acaccgtgac cttaaagcga gtaacattct cctggatgct 1440
 9697 gatatgaatc ctaaaattgc tgattttgga atggcaagga tctttggaat ggatcaaacc 1500
 9699 cagcagaaca caagcagaat agttggtacc tacggttaca tgtctcctga atatgcatg 1560
 9701 cgtggccagt tctcaatgaa atctgatgtc tatagtttcg gagtgttagt tcttgagatt 1620
 9703 ataagcggta ggaagaacaa cagctttatc gagacagatg acgcacagga cttggtgaca 1680
 9705 catgtaagtt taaaggaaag gagttatata tatgcttggg ggctttggag aaacggaaca 1740
 9707 gcgttagacc tcgtggatcc attcattgca gatagttgcc ggaagagtga agtggttcga 1800
 9709 tgcaccata tcggtctttt atgtgttcaa gaagatcctg taaaacgtcc agccatgtca 1860
 9711 accatttccg tgatgtcac tagtaataca atggctttac cagcgcctca gcaaccaggg 1920
 9713 ttttttgtaa ggagtagacc tggaacaaac cggcttgatt cagatcaatc aacgaccaac 1980
 E--> 9715 aagtctgtta cagtatctat tgacgataag tcaatgtctg atttagatcc tcgttga (2040) 2037

10458 <210> SEQ ID NO: 215

10459 <211> LENGTH: 2097

10460 <212> TYPE: DNA

10461 <213> ORGANISM: Arabidopsis thaliana

10463 <400> SEQUENCE: 215

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RAW SEQUENCE LISTING
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Input Set : D:\382636.txt

Output Set: N:\CRF3\07302001\I887272.raw

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10464 atggaatttg cttcgccgga acaacgtcgt ctcgaaacca ttcgatctca catcgatact      60
10466 tctccgacca acgatcaatc atcatctcta ttctcaacg ccaccgcttc ttctgcttca      120
10468 cctttcttta aagaggatag ctacagtgtt gtgcttcag aaaagcttga tactggaaaa      180
10470 tggaaatgtct acagatctaa aagatcgctt acgaaactcg ttagtagggt cccggatcat      240
10472 cctgaaatcg ggactttaca tgacaatttt gtacatgctg ttgaaacata tgctgaaaac      300
10474 aagtatcttg gtacacgagt tcggtccgat ggaaccattg gagagtattc atggatgaca      360
10476 tatggagaag cagcgtctga gcgacaagcc attggttcag gactcttggt tcatggaggt      420
10478 aaccaaggag attgcggttg actctatatt attaacagac cagagtgggt ggttggtgat      480
10480 catgcttggt cagcatattc atttgtctct gtctctttat atgatacact tgggtccagac      540
10482 gctgttaagt ttgtggtgaa tcatgctaatt ctgcaagcta tattttgtgt accacaaacc      600
10484 ttgaatattg taattgctaa gcttcctagc ggaaatccca tccattcgct tcattgtggg      660
10486 gctgatgagc atttgccatc acttctctga ggaactggag tcacaattgt atcataccaa      720
10488 aagctattga gtcagggtcg aagtgaatta catccatttt cgcctccaaa gccagaagac      780
10490 attgcaacca tatgctacac aagtgaacc acagaaacac caaagggtgt tgtgttgact      840
10492 catggaaact tgatcgcgaa tgtcgctggt tccagtgtgg aagcagaatt ctttccttca      900
10494 gatgtttaca tatcatatct tcctttggcg cacatatatg aacgtgcaaa tcagattatg      960
10496 ggggtgtatg gtggtgttgc tgtcggtttc tatcaggggg atgtcttcaa gctgatggat      1020
10498 gattttgctg tgttaagacc aacaatattc tgtagtgtcc ctcgcttata taatcgaata      1080
10500 tatgatggca ttacaagtgc cgtaaaatca tctggggttg tgaaaaaaag gcttttcgaa      1140
10502 attgcttata actcaaagaa gcaagcgatc attaatgggc ggactccttc tgcattttgg      1200
10504 gacaagctgg tgttcaacaa aataaaagaa aagcttgggt gacgggttcg gtttatgggg      1260
10506 tctggtgctt ctctttgtc acctgatgtc atggatttct tgagaatatg ctttggatgt      1320
10508 tcggtgcgtg aagggtatgg tatgaccgag acttcttgtg tcataagtc tatggatgat      1380
10510 ggtgacaatt tatctggcca tgtcggttcc cctaateccag cttgcgaggt aaaacttgtg      1440
10512 gatgttcccg aaatgaatta cacatcagac gatcaacat acccagctgg tgaaatctgt      1500
10514 gtaagaggac caatcatctt caaaggctac tacaagatg aagaacaaac gagagaaatt      1560
10516 cttgatggag atggctggct acacacagga gatatcgggt tgtggttacc tgggtggtcgg      1620
10518 ctcaagatca tagacaggaa gaagaacata ttttaagttg cgcaaggaga atatatagca      1680
10520 ccagagaaga tcgaaaatgt ttataccaaa ttagattcgt tttcgcatg tttcattcac      1740
10522 ggtgatagct tcaattctc tctagtagct atagtttcag tcgaccccg agttatgaaa      1800
10524 gattgggctg catcagaagg catcaagtat gagcatctag gacagctctg taacgatcca      1860
10526 agagtgcgaa agactgttct tgcgtagatg gatgacctg gaagagaagc tcagttgaga      1920
10528 ggggtttgag ttgcaaaggc tgtgtacttt gtgccagaac cattcacctt ggagaatgga      1980
10530 cttctcacac caacattcaa gataaagaga cctcaagcaa aagcctactt tgcagaagca      2040
E--> 10532 attagcaaaa tgtatgcgga aatcgcagcc tcgaacccca ttcttcttaa actgtga      (2100) 2097
10678 <210> SEQ ID NO: 219
10679 <211> LENGTH: 414
10680 <212> TYPE: DNA
10681 <213> ORGANISM: Arabidopsis thaliana
10683 <400> SEQUENCE: 219
10684 atgcaaggaa cgatttcttg tgcaagaaat tataacatga cgacaaccgt cggggaatct      60
10686 ctgcggccgc tatcgcttaa aacgcaggga aacggcgaga gagttcggat ggtggtggag      120
10688 gagaacgcgg tgattgtgat tggacggaga ggatgttgca tgtgtcatgt ggtgaggagg      180
10690 ctgcttcttg gacttgaggt gaatccggcg gtccttgaga ttgatgagga gagggaaagat      240
10692 gaagttttga gtgagttgga gaatattgga gttcaaggcg gcggaggtac ggtgaagtta      300
10694 ccggcggttt atgtaggag gaggtgttt ggagggttag atagggttat ggctactcat      360
E--> 10696 atctccggtg agttagtcc aattcttaag gaagttgggg ctctgtggtt gtga      (420) 414
E--> 12114 <210> SEQ ID NO: 246-247 seg 245 minus
E--> 13296 <210> SEQ ID NO: 270 seg 268-269 minus

```

RAW SEQUENCE LISTING
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DATE: 07/30/2001
TIME: 11:31:17

Input Set : D:\382636.txt
Output Set : N:\CRF3\07302001\I887272.raw

E--> 13720 <210> SEQ ID NO: 279
E--> 14344 <210> SEQ ID NO: 294
E--> 15135 <210> SEQ ID NO: 312
E--> 15535 <210> SEQ ID NO: 321
E--> 15590 <210> SEQ ID NO: 323
E--> 16069 <210> SEQ ID NO: 333
E--> 16131 <210> SEQ ID NO: 336
E--> 16690 <210> SEQ ID NO: 350
E--> 17107 <210> SEQ ID NO: 362
E--> 17397 <210> SEQ ID NO: 369
E--> 18195 <210> SEQ ID NO: 380
E--> 21063 <210> SEQ ID NO: 457
E--> 21826 <210> SEQ ID NO: 479
E--> 26415 <210> SEQ ID NO: 565
E--> 26495 <210> SEQ ID NO: 569
E--> 27326 <210> SEQ ID NO: 593
E--> 28750 <210> SEQ ID NO: 626
E--> 29458 <210> SEQ ID NO: 645
E--> 31195 <210> SEQ ID NO: 683
E--> 32073 <210> SEQ ID NO: 705
E--> 34516 <210> SEQ ID NO: 761
E--> 41007 <210> SEQ ID NO: 899
E--> 43542 <210> SEQ ID NO: 969

*see pp. 33-34 for missing
sequences*

43543 <211> LENGTH: 27
43544 <212> TYPE: DNA
43545 <213> ORGANISM: Artificial Sequence
43547 <220> FEATURE:
43548 <223> OTHER INFORMATION: a primer

OK 43550 <400> SEQUENCE: 962
43551 caatggcttt ggtcctccac tggtcag

E--> 44010 <210> SEQ ID NO: 1954
45664 <210> SEQ ID NO: 1977

seqs 1001 through 1953 missing

45665 <211> LENGTH: 1563
45666 <212> TYPE: RNA
45667 <213> ORGANISM: Nicotiana tabacum
45669 <400> SEQUENCE: 1977

It's not allowed in an RNA sequence.

E--> 45670 ggcacgagat taaactcaca ttcttgatta tcatcttcaa tggattcaaa gcaatcatca 60
E--> 45672 gaattagtgt tcacagtaag gagacaaaag ccagagctaa tagctccggc aaaaccaact 120
E--> 45674 ccacgtgaaa ctaagtttct ttctgatatt gatgatcaag aaggctctcg atttcaaatt 180
E--> 45676 cccgttatte aattttacca taaggattct tctatgggaa ggaaagatcc tgtaaagggt 240
E--> 45678 attaaaaagg ctatagctga aacacttggt ttttactatc catttgctgg ccgtctccgg 300
E--> 45680 gaaggaaatg gccggaaact gatggtggat tgtaccggcg aggggattat gtttgtcgaa 360
E--> 45682 gcggatgctg atgttacact tgagcaattt ggagatgaac ttcagcctcc atttccatgc 420
E--> 45684 ttagaagaac ttctttatga tgttcctgac tctgctggag ttcttaattg ccctttgctt 480
E--> 45686 cttattcagg taactcgtct aagatgtggt ggttttatct tcgcgctaag attaaaccac 540
E--> 45688 acaatgagtg atgcaccagg tcttggtccaa tttatgaccg cagtgggtga aatggcacgc 600
E--> 45690 ggtggatctg ctccatctat acttccagtc tgggtgctgag aattgctaaa tgccagaaat 660
E--> 45692 ccgccccaa tgacatgtac acatcacgaa tacgatgaag tacgcgatac aaagggtaca 720
E--> 45694 attatccct tagacgacat ggttcacaaa tctttctttt ttggcccttc tgaagtctca 780

*Use
"u"
instead.*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/887,272

DATE: 07/30/2001
TIME: 11:31:20

Input Set : D:\382636.txt
Output Set: N:\CRF3\07302001\I887272.raw

It's not allowed

```

E--> 45696 gcacttcgtc gatttgctcc tcatacattg cgtaagtgtt ccacttttga actgctcaca      840
E--> 45698 gcagtccttt ggcgttgctg aacaatgtcc ctaaaacctg atccagaaga ggaagtctgc      900
E--> 45700 gctctttgca ttgtcaatgc acgttcgagg ttcaatcctc ctttgcttac tggctactac      960
E--> 45702 ggcaacgcct ttgcattccc tgtagcagtc acaactgcgg ctaaactgag caaaaatcca     1020
E--> 45704 ctaggatatg cactcgagtt agtgaagaaa acaaagtcgg atgtgacaga agaatatatg     1080
E--> 45706 aaatctgttg cagatttaac ggtgttaaaa ggtagacccc attttacagt ggtgaggact     1140
E--> 45708 tttcttgatg cagatgtgac tagaggtgga tttggagaag tggatttttg atggggaaaa     1200
E--> 45710 gcagtttatg gtggaccagc taaaggagga gtaggtgcaa ttcctggtgt ggctagtttt     1260
E--> 45712 tatataccat ttaaaaacaa gaaaggtgag aatggaattg tggttccaat ttgtttgcct     1320
E--> 45714 ggttttgcaa tggaacatt cgtcaaagaa cttgatggtg tggtgaaagt tgatgctcca     1380
E--> 45716 ttagtcaact caaactatgc cattatcaga cctgcccttt gagatattaa ttatgtcgaa     1440
E--> 45718 tacttttttt taataccacg attaaaggcc atagagtttg tcttcagtcg catatactcg     1500
E--> 45720 gcgtaatttc cttctgattt tatgtgtatg tagtttcaaa tgttgtaagt ttgctctttt     1560
E--> 45722 atc
E--> 49890 <210> SEQ ID NO: 2000

```

> Seqs 1981 through 1999 missing

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

FJI

<400> 68

(sep 30)

atgggagatg	ggactgagtt	tgtgggttagg	tcagataggg	aagataagaa	gcttgctgag	60
gatagaatta	gtgatgagca	agtagtgaag	aatgagttgg	tgagatctga	tgaagtaagg	120
gatgataacg	aggacgaggt	ttttgaggaa	gcgattgggt	cagagaatga	tgagcaggag	180
gaggaggagg	atccaaaacg	tgaattgttt	gaatctgatg	atttgccttt	agtggaaact	240
cttaaaagtt	ctatggttga	gcatgaagtg	gaggattttg	aagaggcagt	gggtgatttg	300
gatgaaacga	gtagcaatga	aggggggtgt	aaagatttta	cggctgttgg	agagagccat	360
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ggaggtggag	gtggttctta	tgataaagtt	gaatcgagct	tggatgttgt	tgataccact	480
gagaatgcta	catcaactaa	tactaatggg	tccaatttag	cagctgagca	tgtgggtatt	540
gaaaacggaa	agactcattc	ttttttggga	aatggaatcg	cctctcctaa	aaataaagaa	600
gtggtggctg	aagttatccc	taaagatgat	gggattgagg	aaccatggaa	tgatggcatt	660
gaagtcgata	attgggagga	aagagttgat	ggcatacaga	cagaacaaga	ggttgaggaa	720
ggtgaaggaa	caactgaaaa	tcaatttgag	aaacggacag	aagaagaggt	tgtagaaggt	780
gaaggaacaa	gtaagaatct	atttgagaaa	cagacagaac	aagatgttgt	ggaaggtgaa	840
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gacaatgaag	tatcaagtgc	tgtgacttca	tctccattgg	aggaatctag	ttccggggaa	1020
aaggggagaga	ctgaagggga	cagtacttgt	ttaaaaccag	agcaacactt	ggcttcttcg	1080
ccgcactcat	atcctgagtc	aactgaagtt	cacagcaata	gtggctcccc	tggggtaact	1140
agtagagaac	acaaccagtt	tcaaagtgtc	aatggaggac	atgatgttca	gagtcctcaa	1200
ccaaataagg	agcttgagaa	gcagcaaagc	agcagagtac	atgtagatcc	agagattaca	1260
gaaaattcac	atgtggaaac	agaacctgag	gtagtaagtt	ctgtttcacc	aacagagtct	1320
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aatcagtttc	agcaagctga	agactctacc	actacagagg	ctgatgagca	tgatgagacc	1500
cgcgagaagc	tccagttgat	cagggtaaaa	tttttgaggc	ttgcacatag	actagggcaa	1560
accccgcata	atgttgttgt	tgctcaggtt	ttatacaggc	ttggattggc	tgagcagttg	1620
aggggcagaa	atggaagccg	tgttggtgct	tttagttttg	atcgcgctag	tgccatggca	1680

gaacagcttg aggctgctgg acaggatcca cttgattttt cttgtacgat tatggttctc	1740
ggaaaaagtg gggttggtaa aagtgaacg atcaattcta tatttgatga agtgaaattt	1800
tgtactgatg cattccagat ggggacaaag agggttcaag atgttgaggg tttggttcag	1860
ggaattaagg tacgggtgat tgacactccc ggtctcttac cttcctgggc tgatcaagcc	1920
aagaatgaga agatcctgaa ttctgttaag gctttcatca agaagaatcc acctgacatt	1980
gtactatata ttgatagggt ggatatgcaa agcagagatt ctggtgacat gcctctcctg	2040
cgcaccataa gtgatgtttt tggctcctcg atatggttta atgccattgt gggtttgact	2100
catgccgctt ctgttccacc agatggcca aatggcactg cttctagcta tgatatgttt	2160
gttacacaac gttctcatgt catccagcag gccattcgcc aagcagctgg agatatgagg	2220
ctcatgaacc ctgtttcttt agttgagaat cactcagctt gcaggactaa tcgggcagggc	2280
cagagagtat taccgaatgg ccaagtgtgg aagccacatt tgttgctact ctcatattgca	2340
tctaagattc tagcagaagc aaatgctctt ttgaagttgc aagataatat tccagggaga	2400
ccatttgca ctcgggtccaa ggctccgcca ttaccatttc tcctttcatc gcttctgcaa	2460
tcaagaccac aacctaagct tcctgaacag cagtatgggt atgaagaaga tgaagatgat	2520
ttagaagaat catcagattc agacgaagaa tcagagtatg atcagcttcc tccgtttaag	2580
agtttgacta aagctcagat ggctacgctt agtaaacttc agaagaagca gtatctcgat	2640
gaaatggagt accgagagaa acttttaatg aagaagcaaa tgaaagagga aagaaagaga	2700
cgtaagatgt ttaagaaatt tgctgcagag attaaagatt tgcctgatgg gtatagtga	2760
aatgtggaag aggagagtgg tggacctgca tcagttccag ttcctatgcc agatttatct	2820
ctacctgctt cttttgactc tgataaccct actcaccgct accggtacct tgattcctcc	2880
aatcagtggc ttgttaggcc agtcttgaa actcatgggt gggatcatga tattggttat	2940
gaaggtgtga atgcagaacg gctctttgtt gtaaaagaaa aaataccaat atctgtctca	3000
ggtcaagtga caaaagacaa gaaggatgca aatgtgcagc tagaaatggc cagctcgggt	3060
aaacatggag agggtaaata aacttccta ggtttcgaca tgcaaactgt tggaaaggaa	3120
ttggcttata ctcttcgaag cgaaacgaga tttacaatt tcaggagaaa caaggctgca	3180
gctggtcttt ctgtaacaca cttgggtgat tcggtttctg cggggttgaa agtcgaagat	3240
aagtttattg ctagtaaata gttcagaatc gtaatgtctg gtggagctat gactagtcgg	3300
ggagattttg cttatggtgg tactttggaa gctcagttga gagataaaga ttatccgctt	3360
ggtcggtttt tgactactct tggactttct gtaatggatt ggcacggtga tcttgctatt	3420

ggaggggaaca tacagtctca ggttcccatt ggacgttctt ctaatttaatt tgctcgtgct 3480

aatctgaaca atagaggagc agggcaagta agtggttcgtg ttaacagctc cgagcagctc 3540

caacttgcta tggttgcgat tgttcctctc ttcaagaagc tacttagtta ttattaccgc 3600

caaacgcaat atggacaatg 3621

Sequence 69 missing

<210> 70

Examples of other missing sequences:
 87, 96, 105, 146, 147, 149, 155, 157,
 161, 167, 245, 268-269, 276-278, 293,
 311, 320, 322, 332, 335, 349, (see
 pp 31-34
 for more)

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/887,272

DATE: 07/30/2001

TIME: 11:32:05

Input Set : D:\382636.txt

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L:23 M:270 C: Current Application Number differs, Replaced Current Application No
L:23 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:124 M:254 E: No. of Bases conflict, LENGTH:Input:1401 Counted:1400 SEQ:2
L:124 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1401 Found:1400 SEQ:2
L:341 M:254 E: No. of Bases conflict, LENGTH:Input:1041 Counted:1040 SEQ:7
L:341 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1041 Found:1040 SEQ:7
L:450 M:254 E: No. of Bases conflict, LENGTH:Input:411 Counted:410 SEQ:10
L:450 M:252 E: No. of Seq. differs, <211>LENGTH:Input:411 Found:410 SEQ:10
L:491 M:254 E: No. of Bases conflict, LENGTH:Input:1011 Counted:1010 SEQ:11
L:491 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1011 Found:1010 SEQ:11
L:705 M:254 E: No. of Bases conflict, LENGTH:Input:2421 Counted:2420 SEQ:15
L:705 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2421 Found:2420 SEQ:15
L:870 M:254 E: No. of Bases conflict, LENGTH:Input:321 Counted:320 SEQ:20
L:870 M:252 E: No. of Seq. differs, <211>LENGTH:Input:321 Found:320 SEQ:20
L:901 M:254 E: No. of Bases conflict, LENGTH:Input:720 Counted:717 SEQ:21
L:1273 M:254 E: No. of Bases conflict, LENGTH:Input:1440 Counted:1434 SEQ:33
L:1791 M:254 E: No. of Bases conflict, LENGTH:Input:2631 Counted:2630 SEQ:39
L:1791 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2631 Found:2630 SEQ:39
L:2133 M:254 E: No. of Bases conflict, LENGTH:Input:1881 Counted:1880 SEQ:45
L:2133 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1881 Found:1880 SEQ:45
L:2445 M:254 E: No. of Bases conflict, LENGTH:Input:1620 Counted:1617 SEQ:49
L:2576 M:254 E: No. of Bases conflict, LENGTH:Input:660 Counted:654 SEQ:52
L:2728 M:254 E: No. of Bases conflict, LENGTH:Input:2061 Counted:2060 SEQ:54
L:2728 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2061 Found:2060 SEQ:54
L:2833 M:254 E: No. of Bases conflict, LENGTH:Input:1080 Counted:1077 SEQ:57
L:2970 M:254 E: No. of Bases conflict, LENGTH:Input:3861 Counted:3860 SEQ:58
L:2970 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3861 Found:3860 SEQ:58
L:3300 M:254 E: No. of Bases conflict, LENGTH:Input:771 Counted:770 SEQ:64
L:3300 M:252 E: No. of Seq. differs, <211>LENGTH:Input:771 Found:770 SEQ:64
L:3396 M:254 E: No. of Bases conflict, LENGTH:Input:1680 Counted:1674 SEQ:66
L:3566 M:254 E: No. of Bases conflict, LENGTH:Input:3621 Counted:3620 SEQ:68
L:3566 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3621 Found:3620 SEQ:68
L:3569 M:214 E: (33) Seq.# missing, SEQ ID NO:69
L:3621 M:254 E: No. of Bases conflict, LENGTH:Input:1401 Counted:1400 SEQ:70
L:3621 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1401 Found:1400 SEQ:70
L:3686 M:254 E: No. of Bases conflict, LENGTH:Input:1740 Counted:1734 SEQ:71
L:4189 M:254 E: No. of Bases conflict, LENGTH:Input:1740 Counted:1737 SEQ:80
L:4273 M:254 E: No. of Bases conflict, LENGTH:Input:1020 Counted:1017 SEQ:82
L:4306 M:254 E: No. of Bases conflict, LENGTH:Input:741 Counted:740 SEQ:83
L:4306 M:252 E: No. of Seq. differs, <211>LENGTH:Input:741 Found:740 SEQ:83
L:4450 M:214 E: (33) Seq.# missing, SEQ ID NO:87
L:4644 M:254 E: No. of Bases conflict, LENGTH:Input:3261 Counted:3260 SEQ:90
L:4644 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3261 Found:3260 SEQ:90
L:4866 M:214 E: (33) Seq.# missing, SEQ ID NO:96
L:4920 M:254 E: No. of Bases conflict, LENGTH:Input:1491 Counted:1490 SEQ:97
L:4920 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1491 Found:1490 SEQ:97
L:5262 M:214 E: (33) Seq.# missing, SEQ ID NO:105
L:5294 M:254 E: No. of Bases conflict, LENGTH:Input:801 Counted:800 SEQ:106

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L:5294 M:252 E: No. of Seq. differs, <211>LENGTH:Input:801 Found:800 SEQ:106
 L:5637 M:254 E: No. of Bases conflict, LENGTH:Input:1620 Counted:1614 SEQ:113
 L:6306 M:254 E: No. of Bases conflict, LENGTH:Input:1401 Counted:1400 SEQ:124
 L:6306 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1401 Found:1400 SEQ:124
 L:6351 M:254 E: No. of Bases conflict, LENGTH:Input:1140 Counted:1137 SEQ:125
 L:6613 M:254 E: No. of Bases conflict, LENGTH:Input:1641 Counted:1640 SEQ:131
 L:6613 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1641 Found:1640 SEQ:131
 L:6731 M:254 E: No. of Bases conflict, LENGTH:Input:1080 Counted:1074 SEQ:133
 L:7301 M:254 E: No. of Bases conflict, LENGTH:Input:360 Counted:357 SEQ:145
 L:7304 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 146 thru 147
 L:7351 M:214 E: (33) Seq.# missing, SEQ ID NO:149
 L:7534 M:214 E: (33) Seq.# missing, SEQ ID NO:155
 L:7577 M:214 E: (33) Seq.# missing, SEQ ID NO:157
 L:7637 M:254 E: No. of Bases conflict, LENGTH:Input:1680 Counted:1674 SEQ:158
 L:7749 M:254 E: No. of Bases conflict, LENGTH:Input:1740 Counted:1734 SEQ:160
 L:7752 M:214 E: (33) Seq.# missing, SEQ ID NO:161
 L:7975 M:214 E: (33) Seq.# missing, SEQ ID NO:167
 L:8032 M:254 E: No. of Bases conflict, LENGTH:Input:471 Counted:470 SEQ:169
 L:8032 M:252 E: No. of Seq. differs, <211>LENGTH:Input:471 Found:470 SEQ:169
 L:8055 M:254 E: No. of Bases conflict, LENGTH:Input:471 Counted:470 SEQ:170
 L:8055 M:252 E: No. of Seq. differs, <211>LENGTH:Input:471 Found:470 SEQ:170
 L:8261 M:254 E: No. of Bases conflict, LENGTH:Input:720 Counted:717 SEQ:174
 L:8438 M:254 E: No. of Bases conflict, LENGTH:Input:531 Counted:530 SEQ:179
 L:8438 M:252 E: No. of Seq. differs, <211>LENGTH:Input:531 Found:530 SEQ:179
 L:8560 M:254 E: No. of Bases conflict, LENGTH:Input:1221 Counted:1220 SEQ:181
 L:8560 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1221 Found:1220 SEQ:181
 L:8726 M:254 E: No. of Bases conflict, LENGTH:Input:1080 Counted:1074 SEQ:185
 L:8852 M:254 E: No. of Bases conflict, LENGTH:Input:771 Counted:770 SEQ:189
 L:8852 M:252 E: No. of Seq. differs, <211>LENGTH:Input:771 Found:770 SEQ:189
 L:9013 M:254 E: No. of Bases conflict, LENGTH:Input:1611 Counted:1610 SEQ:192
 L:9013 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1611 Found:1610 SEQ:192
 L:9715 M:254 E: No. of Bases conflict, LENGTH:Input:2040 Counted:2037 SEQ:204
 L:10195 M:254 E: No. of Bases conflict, LENGTH:Input:2481 Counted:2480 SEQ:210
 L:10195 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2481 Found:2480 SEQ:210
 L:10420 M:254 E: No. of Bases conflict, LENGTH:Input:1761 Counted:1760 SEQ:213
 L:10420 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1761 Found:1760 SEQ:213
 L:10455 M:254 E: No. of Bases conflict, LENGTH:Input:831 Counted:830 SEQ:214
 L:10455 M:252 E: No. of Seq. differs, <211>LENGTH:Input:831 Found:830 SEQ:214
 L:10532 M:254 E: No. of Bases conflict, LENGTH:Input:2100 Counted:2097 SEQ:215
 L:10696 M:254 E: No. of Bases conflict, LENGTH:Input:420 Counted:414 SEQ:219
 L:10775 M:254 E: No. of Bases conflict, LENGTH:Input:2160 Counted:2154 SEQ:220
 L:10984 M:254 E: No. of Bases conflict, LENGTH:Input:831 Counted:830 SEQ:225
 L:10984 M:252 E: No. of Seq. differs, <211>LENGTH:Input:831 Found:830 SEQ:225
 L:12007 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1161 Found:1160 SEQ:242
 L:12114 M:214 E: (33) Seq.# missing, SEQ ID NO:245
 L:12426 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1701 Found:1700 SEQ:250
 L:12630 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1911 Found:1910 SEQ:254
 L:12698 M:252 E: No. of Seq. differs, <211>LENGTH:Input:771 Found:770 SEQ:256
 L:12891 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1581 Found:1580 SEQ:259

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L:13296 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 268 thru 269
L:13720 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 276 thru 278
L:13827 M:252 E: No. of Seq. differs, <211>LENGTH:Input:711 Found:710 SEQ:280
L:13901 M:252 E: No. of Seq. differs, <211>LENGTH:Input:741 Found:740 SEQ:282
L:14344 M:214 E: (33) Seq.# missing, SEQ ID NO:293
L:15132 M:252 E: No. of Seq. differs, <211>LENGTH:Input:981 Found:980 SEQ:310
L:15135 M:214 E: (33) Seq.# missing, SEQ ID NO:311
L:15203 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1881 Found:1880 SEQ:312
L:15535 M:214 E: (33) Seq.# missing, SEQ ID NO:320
L:15590 M:214 E: (33) Seq.# missing, SEQ ID NO:322
L:16037 M:252 E: No. of Seq. differs, <211>LENGTH:Input:501 Found:500 SEQ:330
L:16069 M:214 E: (33) Seq.# missing, SEQ ID NO:332
L:16131 M:214 E: (33) Seq.# missing, SEQ ID NO:335
L:16244 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1341 Found:1340 SEQ:337
L:16374 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2931 Found:2930 SEQ:339
L:16471 M:252 E: No. of Seq. differs, <211>LENGTH:Input:261 Found:260 SEQ:342
L:16690 M:214 E: (33) Seq.# missing, SEQ ID NO:349
L:16761 M:252 E: No. of Seq. differs, <211>LENGTH:Input:711 Found:710 SEQ:351
L:17107 M:214 E: (33) Seq.# missing, SEQ ID NO:361
L:17397 M:214 E: (33) Seq.# missing, SEQ ID NO:368
L:18195 M:214 E: (33) Seq.# missing, SEQ ID NO:379
L:18462 M:252 E: No. of Seq. differs, <211>LENGTH:Input:681 Found:680 SEQ:387
L:18747 M:214 E: (33) Seq.# missing, SEQ ID NO:396
L:18882 M:214 E: (33) Seq.# missing, SEQ ID NO:400
L:18966 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1611 Found:1610 SEQ:403
L:19539 M:252 E: No. of Seq. differs, <211>LENGTH:Input:771 Found:770 SEQ:416
L:20219 M:214 E: (33) Seq.# missing, SEQ ID NO:430
L:20345 M:252 E: No. of Seq. differs, <211>LENGTH:Input:921 Found:920 SEQ:433
L:20608 M:214 E: (33) Seq.# missing, SEQ ID NO:442
L:20636 M:252 E: No. of Seq. differs, <211>LENGTH:Input:711 Found:710 SEQ:443
L:20676 M:214 E: (33) Seq.# missing, SEQ ID NO:445
L:21063 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 455 thru 456
L:21111 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1281 Found:1280 SEQ:457
L:21140 M:252 E: No. of Seq. differs, <211>LENGTH:Input:651 Found:650 SEQ:458
L:21143 M:214 E: (33) Seq.# missing, SEQ ID NO:459
L:21397 M:214 E: (33) Seq.# missing, SEQ ID NO:466
L:21507 M:214 E: (33) Seq.# missing, SEQ ID NO:469
L:21826 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 477 thru 478
L:24180 M:214 E: (33) Seq.# missing, SEQ ID NO:511
L:24238 M:214 E: (33) Seq.# missing, SEQ ID NO:514
L:24458 M:214 E: (33) Seq.# missing, SEQ ID NO:519
L:24680 M:214 E: (33) Seq.# missing, SEQ ID NO:524
L:24850 M:214 E: (33) Seq.# missing, SEQ ID NO:527
L:24921 M:214 E: (33) Seq.# missing, SEQ ID NO:529
L:25089 M:214 E: (33) Seq.# missing, SEQ ID NO:534
L:25228 M:214 E: (33) Seq.# missing, SEQ ID NO:538
L:25676 M:214 E: (33) Seq.# missing, SEQ ID NO:547
L:26107 M:214 E: (33) Seq.# missing, SEQ ID NO:555
L:26209 M:214 E: (33) Seq.# missing, SEQ ID NO:558

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L:26415 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 563 thru 564
L:26495 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 567 thru 568
L:26524 M:214 E: (33) Seq.# missing, SEQ ID NO:570
L:26570 M:214 E: (33) Seq.# missing, SEQ ID NO:573
L:26749 M:214 E: (33) Seq.# missing, SEQ ID NO:579
L:27326 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 591 thru 592
L:27369 M:214 E: (33) Seq.# missing, SEQ ID NO:594
L:27570 M:214 E: (33) Seq.# missing, SEQ ID NO:598
L:27617 M:214 E: (33) Seq.# missing, SEQ ID NO:600
L:28496 M:214 E: (33) Seq.# missing, SEQ ID NO:616
L:28717 M:214 E: (33) Seq.# missing, SEQ ID NO:622
L:28750 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 624 thru 625
L:28861 M:214 E: (33) Seq.# missing, SEQ ID NO:629
L:28929 M:214 E: (33) Seq.# missing, SEQ ID NO:632
L:29224 M:214 E: (33) Seq.# missing, SEQ ID NO:638
L:29458 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 643 thru 644
L:31195 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 681 thru 682
L:32073 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 703 thru 704
L:34516 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 758 thru 760
L:41007 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 896 thru 898
L:43542 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 962 thru 968
L:43550 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:969 differs:962
L:44010 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 1001 thru 1953
L:44034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1955
L:44036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1955
L:44040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1955
L:44073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1957
L:44108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1959
L:44126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1960
L:44150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1961
L:44204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1964
L:44236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1965
L:45670 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:18
L:45672 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:45672 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:28
L:45674 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:22
L:45674 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:50
L:45676 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
L:45676 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:70
L:45678 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
L:45678 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:90
L:45680 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
L:45680 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:104
L:45682 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
L:45682 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:122
L:45684 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:26
L:45684 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:148
L:45686 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:21
L:45686 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:169

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L:45688 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
 L:45688 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:183
 L:45690 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
 L:45690 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:201
 L:45692 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
 L:45692 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:210
 L:45694 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:23
 L:45694 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:233
 L:45696 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:21
 L:45696 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:254
 L:45698 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
 L:45698 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:268
 L:45700 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:21
 L:45700 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:289
 L:45702 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
 L:45702 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:301
 L:45704 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13
 L:45704 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:314
 L:45706 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
 L:45706 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:332
 L:45708 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
 L:45708 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:352
 L:45710 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
 L:45710 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:370
 L:45712 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
 L:45712 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:390
 L:45714 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:19
 L:45714 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:409
 L:45716 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
 L:45716 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:429
 L:45718 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:23
 L:45718 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:452
 L:45720 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:31
 L:45720 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:483
 L:45722 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:45722 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:484
 L:49890 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 1981 thru 1999
 L:49990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2003
 L:50032 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2004
 L:50076 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2005
 L:50294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2006
 L:50302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2006
 L:50312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2006
 L:50314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2006
 L:50318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2006
 L:50322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2006
 L:50324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2006
 L:50326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2006
 L:50418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2007

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L:50420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2007
L:50454 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2008
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L:51228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2020
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L:51344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2022
L:51386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2023
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L:38 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6813) Counted (5727)

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